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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
09/989,890	11/21/2001	Susana Salceda	DEX-0287	1461

32800 7590 06/01/2006

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EXAMINER	
MARTINELL, JAMES	
ART UNIT	PAPER NUMBER
1634	

DATE MAILED: 06/01/2006

Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary	Application No.	Applicant(s)	
	09/989,890	SALCEDA ET AL.	
	Examiner	Art Unit	
	James Martinell	1634	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *27 September 2004*.

2a)☐ This action is **FINAL**. 2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *1-17* is/are pending in the application.

4a) Of the above claim(s) *10-13 and 16* is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *1-9,14,15 and 17* is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☐ The specification is objected to by the Examiner.

10)☐ The drawing(s) filed on _____ is/are: a)☐ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☒ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☒ Information Disclosure Statement(s) (PTO-1449 or PTO/SB/08) Paper No(s)/Mail Date *4/03, 2/04 & 10/04*.
4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____ .
5) ☐ Notice of Informal Patent Application (PTO-152)
6) ☐ Other: _____.

The Art Unit location of your application in the USPTO has changed. To aid in correlating any papers for this application, all further correspondence regarding this application should be directed to Art Unit 1634.

The requirement for restriction mailed July 26, 2004 is vacated and is replaced by the requirement for restriction outlined below.

Restriction to one of the following inventions is required under 35 U.S.C. 121:

I. Claims 1-9, 14/1, 15/1, and 17, drawn to nucleic acids, nucleic acid molecular hybridization assays, vectors, host cells, methods of producing polypeptides, and nucleic acid vaccines, classified in class 536, subclass 23.1, class 435, subclasses 6, 320.1, 325, and 69.1, and class 514, subclass 44.

II. Claims 10, 11, 14/11, and 15,11, drawn to polypeptides, and polypeptide vaccines, classified in class 530, subclass 350 and class 514, subclass 12.

III. Claims 12, 13, and 16, drawn to antibodies, antibody assays, and methods of treatment using antibodies, classified in class 530, subclass 387.1, class 435, subclass 7.1, and class 424, subclass 130.1.

The inventions are independent or distinct, each from the other for the following reasons. The nucleic acids, vectors, host cells, and nucleic acid vaccines of Group I are materially different from, and are therefore independent and distinct from the polypeptides and polypeptide vaccines of Group II and the antibodies of Group III. The methods of Group I may be practiced independently of the methods of Group III. The nucleic acids, vectors, host cells, and nucleic acid vaccines of Group I are not needed to practice the methods of Group III. The polypeptides and polypeptide vaccines of Group II are materially different from, and are therefore independent and distinct from the antibodies of Group III. The polypeptides and polypeptide vaccines of Group II are not needed to practice the methods of Group III.

Claims 1-9, 14/1, 15/1, and 17 are drawn to nucleotides, nucleotide constructs, and/or methods requiring the use of nucleotides or nucleotide constructs that contain more than one individual, independent, and distinct nucleotide sequence in alternative form. Accordingly, these claims are subject

to restriction under 35 U.S.C. § 121 as outlined in 1192 O.G. 68 (November 19, 1996). This notice permits the examination of from one to ten independent and distinct nucleotide sequences in a single application based upon USPTO resources.

Applicant is required to select no more than ONE of the individual sequences for examination. The search of the no more than ONE selected sequence may include the complement of the selected sequence and, where appropriate, may include subsequences within the selected sequence (*e.g.,* oligomeric probes and/or primers).

Claims 10-13, 14/11, 15/11, and 16 are drawn to more than one unrelated, independent, and distinct polypeptide or methods requiring the use of more than one unrelated, independent, and distinct polypeptide. Should applicants elect either one of Groups II or III for examination, applicants are further required to select one polypeptide or a set of methods that requires the use of only one polypeptide for examination on the merits.

Applicants have elected original Group I (claims 1-5, 7, and 8) and SEQ ID NO: 105 encoding SEQ ID NO: 238 for examination in the response filed September 27, 2004. Applicants should note that the requirement for restriction is among independent and distinct inventions and that there is no species election. In order to expedite prosecution of the application, applicants' election of Group I will result in the examination of claims 1-9, 14/1, 15/1, and 17 as they pertain to SEQ ID NO: 105 and nucleic acids that encode SEQ ID NO: 238 or portions thereof in this Office action. Applicants may traverse the requirement for restriction in this Office action in their next response.

Claims 10-13, 14/11, 15/11, and 16 are withdrawn from further consideration pursuant to 37 CFR 1.142(b), as being drawn to a nonelected invention, there being no allowable generic or linking claim. Applicant timely traversed the restriction (election) requirement in the reply filed on September 27, 2004.

The following is a quotation of the first paragraph of 35 U.S.C. 112:

> The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

The following is a quotation of the second paragraph of 35 U.S.C. 112:

> The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

Claims 1-9, 14, 15, and 17 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention. the claims are vague, indefinite, and incomplete.

(a) Claim 1 is vague and indefinite because it claims more than was elected.

(b) The recitation of "comprising a nucleic acid sequence" (claim 1(a) and 1(b)) is vague and indefinite because it is not clear whether applicant intends the phrase to include the entire nucleic acid sequence of SEQ ID NO: 105 or to include all nucleic acids that may include "a" sequence as short as two contiguous nucleotides of SEQ ID NO: 105.

(c) The recitation of "encodes an amino acid sequence" (claims 1(a)) is vague and indefinite because it is not clear whether applicant intends the phrase to include nucleic acids that encode the entire amino acid sequence of SEQ ID NO: 238 or to include all nucleic acids that may encode an amino acid sequence that includes "a" sequence as short as two contiguous amino acids of SEQ ID NO: 238.

(d) The recitation of "selectively hybridizes" (claim 1) is vague and indefinite because selective hybridization depends upon the presence of competing binding partners in the reaction mixture. There is no mention of the presence or absence of such competing binding partners in the claims.

(e) The recitation of "will selectively hybridize" (claim 6) is vague and indefinite because selective hybridization depends upon the presence of competing binding partners in the reaction mixture. There is no mention of the presence or absence of such competing binding partners in the claims.

(f) The recitation of "means for determining the presence of the nucleic acid molecule of claim 1" (claim 15) is vague and indefinite because the nature of such "means" is not disclosed or mentioned. The function of "determining the presence of the nucleic acid of claim 1" is so broad as to make the metes and bounds of the "means" for performing the function unclear.

(g) Claims 14, 15, and 17 are vague, indefinite, and incomplete because they depend from non-elected claim 11.

Claims 1-9, 14, 15, and 17 are rejected under 35 U.S.C. 112, first paragraph, as failing to comply with the written description requirement. The claim(s) contains subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention. The claimed invention is not described adequately in that the claims are broad enough to include any and all nucleic acids that comprise either as few as two contiguous nucleotides of SEQ ID NO: 105 or encode as few as two amino acids of SEQ ID NO: 238 (see items (b) and (c) in the rejection above).

The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

> A person shall be entitled to a patent unless –
>
> (a) the invention was known or used by others in this country, or patented or described in a printed publication in this or a foreign country, before the invention thereof by the applicant for a patent.
>
> (b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.

Claims 1-3, 7, and 8 are rejected under 35 U.S.C. 102(b) as being clearly anticipated by Puttikhunt et al (Molec. Gen. Genet. 247: 118 (1995)). Puttikhunt et al discloses a DNA that encodes amino acids 51-60 of SEQ ID NO: 238 (see the alignment below). Thus, the DNA of Puttikhunt et al is embraced by the claims (*e.g.*, see claim 1(a)).

```
RESULT 32
STMSAM/c
LOCUS       STMSAM                  2981 bp    DNA     linear   BCT 02-SEP-1997
DEFINITION  Streptomyces coelicolor DNA for  aspartate
            aminotransferase,ribosomal protein, partial and complete cds.
ACCESSION   D32254
VERSION     D32254.1  GI:971285
KEYWORDS    nusG; secE; rplK; rplA; ribosomal protein; aspartate
            aminotransferase.
SOURCE      Streptomyces coelicolor A3(2)
  ORGANISM  Streptomyces coelicolor A3(2)
            Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
            Streptomycineae; Streptomycetaceae; Streptomyces.
REFERENCE   1  (bases 1 to 2981)
  AUTHORS   Puttikhunt,C., Nihira,T. and Yamada,Y.
  TITLE     Cloning, nucleotide sequence, and transcriptional analysis of the
            nusG gene of Streptomyces coelicolor A3(2), which encodes a
            putative transcriptional antiterminator
  JOURNAL   Mol. Gen. Genet. 247 (1), 118-122 (1995)
   PUBMED   7715599
REFERENCE   2  (bases 1 to 2981)
  AUTHORS   Puttikhunt,C.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-JUL-1994) Chunya Puttikhunt, Osaka University,
            Department of Biotechnology; 2-1 Yamadaoka, Suita, Osaka 565, Japan
            (Tel:06-877-5111(ex.3441), Fax:06-879-7448)
COMMENT     Submitted (20-Jul-1994) to DDBJ by:
            Puttikhunt Chunya
            Osaka University
            Department of Biotechnology
            2-1 Yamadaoka
            Suita, Osaka 565
            Japan
            Phone: 06-877-5111 x3441
            Fax:   06-879-7448.
DRDKLYAPLEAVRLAKETSTSKFDGTVEV
                    AFRLGVDPRKADQMVRGTVNLPHGTGKTA"
ORIGIN

Alignment Scores:
Pred. No.:              44.2          Length:          2981
Score:                  10.00         Matches:         10
Percent Similarity:     100.0%        Conservative:    0
Best Local Similarity:  100.0%        Mismatches:      0
Query Match:            4.7%          Indels:          0
DB:                     1             Gaps:            0

US-09-989-890-238 (1-212) x STMSAM (1-2981)

Qy         51 GlyAlaGlyLeuProSerAlaSerAlaAla 60
              ||||||||||||||||||||||||||||||
Db       1860 GGCGCCGGCTTGCCCTCGGCCTCGGCGGCC 1831
```

Claims 1-5, 7-9, 15, and 17 are rejected under 35 U.S.C. 102(b) as being clearly anticipated by Williams et al (WO 99/38972 (August 5, 1999). Williams et al discloses a lung cancer marker DNA of 300 nucleotides length that matches with 300 nucleotides of SEQ ID NO: 105. See the alignment of SEQ ID NO: 105 of the instant application with SEQ ID NO: 861 of Williams et al. Thus, SEQ ID NO: 861 of Williams et al meets claim 1(a)-(d). The DNA of Williams et al would selectively hybridize to SEQ ID NO: 105 of the instant application because maximum duplex stability is reached at 25-50 base pairs (see Kennell (Progr. Nucl. Acid Res. Mol. Biol. 11: 259 (1971)) pages 260-261). Williams et al also teaches the use of vectors and transformed host cells for heterologous expression of nucleic acids (*e.g.*, see pages 15-17 of Williams et al) and the use of nucleic acids *in vivo* (see pages 74-76). It is noted here that claim 8 is construed to not include transgenic organisms because of the necessity of the presence of a vector in the host cell and in view of the definition of "host cell" in the application at page 21, first full paragraph.

```
RESULT 12
AAZ13392
ID   AAZ13392 standard; cDNA; 300 BP.
XX
AC   AAZ13392;
XX
DT   12-OCT-1999  (first entry)
XX
DE   Human gene expression product cDNA sequence SEQ ID NO:861.
XX
KW   Human; gene; gene expression product; diagnosis; therapy; probe;
KW   detection; mapping; tissue typing; profiling; forensic; cancer;
KW   genetic analysis; colorectal cancer; breast cancer; lung cancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO9938972-A2.
XX
PD   05-AUG-1999.
XX
PF   28-JAN-1999;   99WO-US001619.
XX
PR   28-JAN-1998;   98US-0072910P.
PR   24-FEB-1998;   98US-0075954P.
PR   31-MAR-1998;   98US-0080114P.
PR   03-APR-1998;   98US-0080515P.
PR   03-APR-1998;   98US-0080666P.
PR   21-OCT-1998;   98US-0105234P.
PR   28-OCT-1998;   98US-0105877P.
XX
PA   (CHIR ) CHIRON CORP.
PA   (HYSE-) HYSEQ INC.
```

XX
PI Williams LT, Escobedo J, Innis MA, Garcia PD, Sudduth-Klinger J;
PI Reinhard C, Giese K, Randazzo F, Kennedy GC, Pot D, Kassam A;
PI Lamson G, Drmanac R, Crkvenjakov R, Dickson M, Drmanac S, Labat I;
PI Leshkowitz D, Kita D, Garcia V, Jones WL, Stache-Crain B;
XX
DR WPI; 1999-494092/41.
XX
PT Novel human genes and their expression products which are differentially
PT expressed in different cell types.
XX
PS Claim 1; Page 860; 2479pp; English.
XX
CC The present invention describes a library of human polynucleotides
CC comprising the sequences given in AAZ12532 to AAZ17779. Also described is
CC a method of detecting differentially expressed genes correlated with the
CC cancerous state of a mammalian cell, comprising detecting at least one
CC differentially expressed gene product in a test sample from a cell
CC suspected of being cancerous, where the gene product is encoded by one of
CC the 5248 polynucleotide sequences given in AAZ12532 to AAZ17779. The
CC polynucleotides can be used as a source of primers and probes, which can
CC be used for a variety of purpose, e.g. detection of expression levels,
CC mapping, tissue typing or profiling, forensics, genetic analysis and
CC detection of polymorphisms. Polypeptides encoded by the polynucleotides
CC can be used for raising antibodies for experimental, diagnostic and
CC therapeutic purposes. The polynucleotides may also be used to construct
CC arrays for diagnostics (which may be used to determine function of an
CC encoded protein); and to detect differences in expression levels between
CC two cells (e.g. to identify abnormal or diseased tissue in a human, to
CC identify a genetic predisposition or susceptibility to a disease such as
CC cancer). The polynucleotides of the invention are especially used in the
CC diagnosis, prognosis and management of colorectal cancer, breast cancer,
CC and lung cancer. The polynucleotides can also be used to screen for
CC peptide analogues and antagonists
XX
SQ Sequence 300 BP; 63 A; 96 C; 90 G; 51 T; 0 U; 0 Other;

Query Match 17.5%; Score 300; DB 2; Length 300;
Best Local Similarity 100.0%; Pred. No. 2.5e-133;
Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy        825 CTCGGACCTTATCAGCAGCATCACGCAGGACTACCACCTGGATGAGCAGGATGCTGAGGG 884
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CTCGGACCTTATCAGCAGCATCACGCAGGACTACCACCTGGATGAGCAGGATGCTGAGGG 60

Qy        885 CCGCCTGGTACGCGGCATCATTCGCATTAGTACCCGAAAGAGCCGTGCTCGCCCACAGAC 944
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CCGCCTGGTACGCGGCATCATTCGCATTAGTACCCGAAAGAGCCGTGCTCGCCCACAGAC 120

Qy        945 CTCGGAGGGTCGTTCAACTCGGGCTGCTGCCCCAACCGCTGCTGCCCCTGACAGTGGCCA 1004
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTCGGAGGGTCGTTCAACTCGGGCTGCTGCCCCAACCGCTGCTGCCCCTGACAGTGGCCA 180

Qy       1005 TGAGACCATGGTGGGCTCAGGTCTCAGCCAGGATGAGCTGACAGTGCAGATCTCCCAGGA 1064
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TGAGACCATGGTGGGCTCAGGTCTCAGCCAGGATGAGCTGACAGTGCAGATCTCCCAGGA 240

Qy       1065 GACGACTGCAGATGCCATCGCCCGGAAGCTGAGGCCTTATGGAGCTCCAGGGTACCCAGC 1124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GACGACTGCAGATGCCATCGCCCGGAAGCTGAGGCCTTATGGAGCTCCAGGGTACCCAGC 300
```

Claims 1-3, 7, and 8 are rejected under 35 U.S.C. 102(a) as being clearly anticipated by GenBank® Accession No. AL592304 (July 25, 2001). GenBank® Accession No. AL592304 discloses a DNA that is 60.5% identical to SEQ ID NO: 105 (see the alignment below). Thus, the DNA of GenBank® Accession No. AL592304 is embraced by the claims. Since the DNA of the reference was sequenced, it was necessarily contained within a vector and host cell (claims 7 and 8). GenBank® Accession No. AL592304 is cited as prior art because there is no basis in Serial No. 60/252,509 for SEQ ID NO: 105.

```
RESULT 9
AL592304
LOCUS       AL592304              111738 bp    DNA     linear   HTG 25-JUL-2001
DEFINITION  Homo sapiens chromosome 1 clone RP3-426N7, 7 unordered pieces.
ACCESSION   AL592304
VERSION     AL592304.1  GI:14586390
KEYWORDS    HTG; HTGS_PHASE1; HTGS_CANCELLED.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Mclay,K.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire,
            CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
            requests: clonerequest@sanger.ac.uk
COMMENT     -------------- Genome Center
            Center: Sanger Centre
            Center code: SC
            Web site: http://www.sanger.ac.uk
            Contact: humquery@sanger.ac.uk
            -------------- Project Information
            Center project name: dJ426N7
            -------------- Summary Statistics
            Assembly program: XGAP4; version 4.5
            Sequencing vector: plasmid; L08752; 100% of reads
            Chemistry: Dye-terminator Big Dye; 100% of reads
            Consensus quality: 110287 bases at least Q40
            Consensus quality: 110500 bases at least Q30
            Consensus quality: 110681 bases at least Q20
            Insert size: 111138; sum-of-contigs
            Insert size: 119403; 8.4% error; agarose-fp
            Quality coverage: 11.23x in Q20 bases; sum-of-contigs Quality
            coverage: 10.67x in Q20 bases; agarose-fp
            --------------.
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 7 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
```

```
            * as soon as it is available and the accession number will
            * be preserved.
            *        1    18058: contig of 18058 bp in length
            *    18059    18158: gap of 100 bp
            *    18159    35144: contig of 16986 bp in length
            *    35145    35244: gap of 100 bp
            *    35245    54710: contig of 19466 bp in length
            *    54711    54810: gap of 100 bp
            *    54811    72936: contig of 18126 bp in length
            *    72937    73036: gap of 100 bp
            *    73037    92888: contig of 19852 bp in length
            *    92889    92988: gap of 100 bp
            *    92989   108739: contig of 15751 bp in length
            *   108740   108839: gap of 100 bp
            *   108840   111738: contig of 2899 bp in length.
FEATURES             Location/Qualifiers
     source          1. .111738
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /chromosome="1"
                     /clone="RP3-426N7"
                     /clone_lib="RPCI-3"
     misc_feature    1. .18058
                     /note="assembly_fragment:02048
                     fragment_chain:1
                     clone_end:T7
                     vector_side:left"
     misc_feature    18159. .35144
                     /note="assembly_fragment:02454
                     fragment_chain:1"
     misc_feature    35245. .54710
                     /note="assembly_fragment:02786
                     fragment_chain:1"
     misc_feature    54811. .72936
                     /note="assembly_fragment:00223
                     fragment_chain:2"
     misc_feature    73037. .92888
                     /note="assembly_fragment:01820
                     fragment_chain:2"
     misc_feature    92989. .108739
                     /note="assembly_fragment:01122
                     fragment_chain:2"
     misc_feature    108840. .111738
                     /note="assembly_fragment:02919
                     fragment_chain:2
                     clone_end:SP6
                     vector_side:right"
ORIGIN

  Query Match             60.5%;  Score 1035.8;  DB 2;  Length 111738;
  Best Local Similarity   99.8%;  Pred. No. 9.7e-250;
  Matches 1037;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ATGCCCCGCCCTGGACACCCCCGCCCAGCATCTGGGCCTCCACGCTTGGGACCGTGGGAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      95726 ATGCCCCGCCCTGGACACCCCCGCCCAGCATCTGGGCCTCCACGCTTGGGACCGTGGGAG 95785

Qy         61 CGGCCAACAGAGCTATGTCTGGAGACATATGATAAACCACCTCAGCCCCCACCAAGCCGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db      95786 CGGCCAACAGAGCTATGTCTGGAGACATATGATAAACCACCTCAGCCCCCACCAAGCCGC 95845

Qy        121 CGCACCCGTAGACCAGACCCCAAGGACCCTGGCCACCATGGGCCAGAGAGCATTACCTTC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      95846 CGCACCCGTAGACCAGACCCCAAGGACCCTGGCCACCATGGGCCAGAGAGCATTACCTTC 95905

Qy        181 ATCTCTGGCTCTGCTGAGCCGGCCCTTGAGTCCCCCACCTGCTGCCTGCTCTGGCGACCC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      95906 ATCTCTGGCTCTGCTGAGCCGGCCCTTGAGTCCCCCACCTGCTGCCTGCTCTGGCGACCC 95965

Qy        241 TGGGTGTGGGAGTGGTGCCGGGCTGCCTTCTGCTTCCGCCGCTGCCGGGATTGCCTCCAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db.     95966 TGGGTGTGGGAGTGGTGCCGGGCTGCCTTCTGCTTCCGCCGCTGCCGGGATTGCCTCCAG 96025

Qy        301 CGCTGTGGAGCCTGTGTGCGGGGATGCAGCCCCTGCCTGTCTACTGAGGACTCCACTGAG 360
              |||||||||||||||||| |||||||||||||||||||||||||||| |||||||||
Db      96026 CGCTGTGGAGCCTGTGTGTGGGGATGCAGCCCCTGCCTGTCTACTGAGGATTCCACTGAG 96085

Qy        361 GGGACTGCTGAAGCCAACTGGGCCAAGGAGCACAATGGAGTGCCCCCCAGCCCTGATCGT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      96086 GGGACTGCTGAAGCCAACTGGGCCAAGGAGCACAATGGAGTGCCCCCCAGCCCTGATCGT 96145

Qy        421 GCACCCCCCAGCCGGCGGGATGGCCAGCGGCTCAAGTCAACCATGGGCAGCAGCTTCAGC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      96146 GCACCCCCCAGCCGGCGGGATGGCCAGCGGCTCAAGTCAACCATGGGCAGCAGCTTCAGC 96205

Qy        481 TACCCCGATGTTAAGCTCAAAGGCATCCCTGTGTATCCCTACCCGAGGGCCACCTCCCCA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      96206 TACCCCGATGTTAAGCTCAAAGGCATCCCTGTGTATCCCTACCCGAGGGCCACCTCCCCA 96265

Qy        541 GCCCCTGATGCGGACTCCTGCTGCAAGGAGCCACTGGCCGATCCCCCACCCATGCGACAC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      96266 GCCCCTGATGCGGACTCCTGCTGCAAGGAGCCACTGGCCGATCCCCCACCCATGCGACAC 96325

Qy        601 AGCCTGCCCAGCACCTTTGCCAGTAGTCCTCGTGGCTCCGAGGAGTACTATTCTTTCCAT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      96326 AGCCTGCCCAGCACCTTTGCCAGTAGTCCTCGTGGCTCCGAGGAGTACTATTCTTTCCAT 96385

Qy        661 GAGTCGGACCTGGACCTGCCGGAGATGGGCAGTGGCTCCATGTCGAGCCGAGAAATTGAT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      96386 GAGTCGGACCTGGACCTGCCGGAGATGGGCAGTGGCTCCATGTCGAGCCGAGAAATTGAT 96445

Qy        721 GTGCTCATCTTCAAGAAGCTGACAGAGCTGTTCAGCGTACACCAGATCGATGAGCTGGCC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      96446 GTGCTCATCTTCAAGAAGCTGACAGAGCTGTTCAGCGTACACCAGATCGATGAGCTGGCC 96505

Qy        781 AAGTGCACATCAGACACTGTGTTCCTGGAGAAGACCAGTAAGATCTCGGACCTTATCAGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      96506 AAGTGCACATCAGACACTGTGTTCCTGGAGAAGACCAGTAAGATCTCGGACCTTATCAGC 96565

Qy        841 AGCATCACGCAGGACTACCACCTGGATGAGCAGGATGCTGAGGGCCGCCTGGTACGCGGC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      96566 AGCATCACGCAGGACTACCACCTGGATGAGCAGGATGCTGAGGGCCGCCTGGTACGCGGC 96625

Qy        901 ATCATTCGCATTAGTACCCGAAAGAGCCGTGCTCGCCCACAGACCTCGGAGGGTCGTTCA 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      96626 ATCATTCGCATTAGTACCCGAAAGAGCCGTGCTCGCCCACAGACCTCGGAGGGTCGTTCA 96685

Qy        961 ACTCGGGCTGCTGCCCCAACCGCTGCTGCCCCTGACAGTGGCCATGAGACCATGGTGGGC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db      96686 ACTCGGGCTGCTGCCCCAACCGCTGCTGCCCCTGACAGTGGCCATGAGACCATGGTGGGC 96745

Qy       1021 TCAGGTCTCAGCCAGGATG 1039
              ||||||||||||||||||
Db      96746 TCAGGTCTCAGCCAGGATG 96764
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Any inquiry concerning this communication or earlier communications from the examiner should be directed to James Martinell whose telephone number is (571) 272-0719.

The examiner works a flexible schedule and can be reached by phone and voice mail. Alternatively, a request for a return telephone call may be e-mailed to james.martinell@uspto.gov. Since e-mail communications may not be secure, it is suggested that information in such requests be limited to name, phone number, and the best time to return the call.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Ram Shukla, can be reached on (571) 272-0735.

OFFICIAL FAX NUMBER

The fax phone number for the organization where this application or proceeding is assigned is (571) 273-8300. Any Official Communication to the USPTO should be faxed to this number.

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James Martinell, Ph.D.
Primary Examiner
Art Unit 1634

5/24/06